

SCORE Search Results Details for Application 10797393 and Search Result 20070118_073132_us-10-797-393a-1.rag.

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This page gives you Search Results detail for the Application 10797393 and Search Result 20070118_073132_us-10-797-393a-1.rag.
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1	2505	100.0	484	5	AAE24207 Aspergillus
2	2505	100.0	484	8	Ady5239 Aspergillus
3	2505	100.0	484	9	Ady5239 Aspergillus
4	2505	100.0	484	9	Ady5239 Aspergillus
5	2505	100.0	484	9	Ady5239 Aspergillus
6	2505	100.0	484	10	Ady5239 Fungal ac
7	2504	98.4	476	9	Ady52195 Aspergillus
8	2510	98.3	476	9	Ady52228 Aspergillus
9	2508	98.2	476	9	Ady52230 Aspergillus
10	2537	98.1	476	9	Ady52232 Aspergillus
11	2537	98.1	476	9	Ady52231 Aspergillus
12	2536	98.1	476	9	Ady52233 Aspergillus
13	2516	98.1	476	9	Ady52227 Aspergillus
14	2516	98.1	476	9	Ady52229 Aspergillus
15	2503	96.8	505	9	Ady256318 Aspergillus
16	2503	96.8	505	9	Ady43752 A. niger
17	2501.5	96.8	477	9	Ady52234 Aspergillus
18	2483	96.1	511	9	Ady25804 A. niger
19	2483	96.1	588	9	Ady72843 Hybrid al
20	2483	96.1	608	9	Ady72339 Hybrid al
21	2483	96.1	609	9	Ady256318 Aspergillus
22	2483	96.1	619	9	Ady72337 Hybrid al
23	2483	96.1	629	9	Ady25810 Hybrid al
24	2483	96.1	640	9	Ady25828 Hybrid al
25	2416	94.2	480	10	AEE61224 A. kawachii
26	2416	94.2	480	10	Ady52512 Aspergillus
27	2436	94.2	619	10	Ady61223 A. kawachii
28	2436	94.2	619	10	Ady57522 A. kawachii
29	2436	94.2	640	10	AEE61214 A. kawachii
30	2436	94.2	640	10	Ady57532 A. kawachii
31	2427	93.9	640	9	Ady21552 Aspergillus
32	2427	93.9	640	9	Ady25817 Aspergillus
33	2427	93.9	640	9	Ady72835 Wild type
34	2420	93.6	619	9	Aed94831 Aspergillus
35	2420	93.6	640	9	Aed94832 Aspergillus
36	1940.5	75.1	630	6	Abb80178 A. fumigata
37	1846	71.4	608	9	Ady25847 Hybrid al
38	1842	71.3	608	9	Ady25851 Hybrid al
39	1839	71.1	608	9	Ady25846 Hybrid al
40	1834	70.9	608	9	Ady25852 Hybrid al
41	1830	70.8	608	9	Ady25853 Hybrid al
42	1826	70.6	608	9	Ady25843 Hybrid al
43	1821	70.4	608	9	Ady25854 Hybrid al
44	1818	70.3	608	9	Ady25849 Hybrid al
45	1817	70.3	608	9	Ady25848 Hybrid al

Database :

A_Geneset8_q:*

1: genesetp1980s:*

2: genesetp1980s:*

3: genesetp2000s:*

4: genesetp2001s:*

5: genesetp2002s:*

6: genesetp2003as:*

7: genesetp2003bs:*

8: genesetp2004s:*

9: genesetp2005s:*

10: genesetp2006s:*

SUMMARIES

Query Score Match Length DB ID Description

http://es/ScoreAccessWeb/GetItem.action?ApplId=10797393&seqId=1052216&itemName=20070118_07... 1/22/2007

ALIGNMENTS					
RESULT 1					
AAE4207	ID	AAE24207 standard	protein:	484 AA.	
XX	XX	XX	XX	XX	XX
AC	AC	AAE24207;			
XX	XX	XX	XX	XX	XX
DT	DT	04-OCT-2002 (first entry)			
XX	XX	Aspergillus niger alpha-amylase protein.			
DS	DS				
KW	KW	Ethanol production; starch; fermentation; liquefaction; alpha-amylase;			
KW	KW	fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.			
OS	OS	Aspergillus niger.			
XX	XX				

Query	Match	Similarity	Length	DB	Score	Best Local	Similarity	Length	DB	Score	Pred.	No.	3..9e-18;																																																																																																																																						
						Matches	484	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;																																																																																																																																				
Qy	1 LSAAWSRTQSIPFLTDRGRTDNSTATCTNTGENEYCGGSQGIGIDHDLYEGMGFTAI	60	60	Db	1 LSAAWSRTQSIPFLTDRGRTDNSTATCTNTGENEYCGGSQGIGIDHDLYEGMGFTAI	60	60	Db	1 WSPTTBOLPODPADEGAHYGYNQKIQYDVNSNFGTADNIKSLSDALHARGMYLMDVYP	120	120	Qy	61 WSPTTBOLPODPADEGAHYGYNQKIQYDVNSNFGTADNIKSLSDALHARGMYLMDVYP	120	120	Db	61 WSPTTBOLPODPADEGAHYGYNQKIQYDVNSNFGTADNIKSLSDALHARGMYLMDVYP	120	120	Qy	121 DHMGYAGNGNDVYDFPDPDSSYRHPCLITDWDNLTVNECDWEGDTIVSPLDQDTE	180	180	Db	121 DHMGYAGNGNDVYDFPDPDSSYRHPCLITDWDNLTVNECDWEGDTIVSPLDQDTE	180	180	Qy	181 TAVKITYWDADIVSNYSVDGLRIDSVLEVQDFPPGTRASGVYCVGEIDNGNPASDC	240	240	Db	181 TAVKITYWDADIVSNYSVDGLRIDSVLEVQDFPPGTRASGVYCVGEIDNGNPASDC	240	240	Qy	241 PYQRKVLGDVNPYKPYKOLYAFESSSSISLNLYMIKSVAASDCSDPTLGNFTENHDNPR	300	300	Db	241 PYQRKVLGDVNPYKPYKOLYAFESSSSISLNLYMIKSVAASDCSDPTLGNFTENHDNPR	300	300	Qy	301 PAKTSDYSSQAKVNLSTPIFSDGIPIVYAGEEHYAGGKPVYNREATWLGDTSAELTT	360	360	Db	301 PAKTSDYSSQAKVNLSTPIFSDGIPIVYAGEEHYAGGKPVYNREATWLGDTSAELTT	360	360	Qy	361 WIATTNAIRKLATAADASAYITYANDAFTDSNTIANAKGTGSQVITLUSNKGSSSYT	420	420	Db	361 WIATTNAIRKLATAADASAYITYANDAFTDSNTIANAKGTGSQVITLUSNKGSSSYT	420	420	Qy	421 LTLSGSGTISCTGKLIETAYCTSVTVDSSGDIYVPMASGLPRLVPLASVYDSSLCLGGSGR	480	480	Db	421 LTLSGSGTISCTGKLIETAYCTSVTVDSSGDIYVPMASGLPRLVPLASVYDSSLCLGGSGR	480	480	Qy	481 LYVE 484			Db	481 LYVE 484			Qy	RESULT 3			Db	ADV09273			XX	ADV09273 standard; protein; 484 AA.			XX	ADV09273;			AC	ADV09273;			DT	24-FEB-2005 (first entry)			XX	Aspergillus niger acid alpha-amylase amino acid sequence - SEQ ID 1.			DE	Aspergillus niger acid alpha-amylase amino acid sequence - SEQ ID 1.			XX	alcohol production ; starch hydrolysis; fuel ethanol; potable ethanol;			KW	industrial ethanol; enzyme; acid alpha-amylase.			XX	Aspergillus niger.			OS	Aspergillus niger.			XX	ADV09273			PP	28-MAY-2004; 2004WO-DK000973.			XX	WD0004106533-A1.			PR	10-MAY-2003; 2003DK-000000812.			XX	(NOVO) NOVOZYMES AS.			PA	(NOVO) NOVOZYMES AS.		

http://es/ScoreAccessWeb/GetItem.action?AppId=0797393&seqId=05226&itemName=20070108_07... 1/22/2007

http://es/ScoreAccessWeb/GelItem.action?AppId=10797393&seqId=1052216&itemName=20070118_07... 1/22/2007

RESULT 4

AEB72807 standard; protein: 484 AA.

ID AEB72807:

DE Fungal acid alpha-amylase.

AC AEB72807:

XX
DT 06-OCT-2005 (first entry)
XX
KW glucoamylase; fermentation; cereals; alcohol; ethanol; fuel ethanol;
potable ethanol; industrial ethanol; gelatinization.
XX
OS Aspergillus niger.

XX
PN WO2005069840-A2.XX
PD 04-AUG-2005.XX
PP 14-JAN-2005; 2005HO-US001147.

PR 16-JAN-2004; 2004US-0537071P.

PR 14-DEC-2004; 2004US-0536013P.

XX
PA (NOVO) NOVOZYMES NORTH AMERICA INC.

PA (NOVO) NOVOZYMES AS.

PI Allain E. Wenger KS, Bisgaard-Frantzen H;
XX
DR WPI: 2005-542205/55.

XX
PT Producing fermentation product e.g. ethanol from starch-containing material involves saccharifying the material with specific glucamylase, at temperature below initial gelatinization temperature of the material and fermenting.
XX
PS Disclosure: SEQ ID NO 3; 96PP; English.

XX
This sequence represents an acid alpha-amylase which was used in the method of the invention. The method for producing a fermentation product from milled starch-containing material involves: saccharifying milled starch-containing material with the glucamylase from the fungi *Athelia rolfsii*, at temperature below the initial gelatinization temperature of starch containing material; and fermenting using a fermenting medium. The process is carried out for 1 - 250, especially 80 - 110 hours, at pH of 3 - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 - 55 (preferably 25 - 40, especially 30 - 35) wt. %. The sugar concentration is kept below 3 wt. % during saccharification and fermentation. A slurry of water and milled starch-containing material is prepared before step (a). The milled starch-containing material is prepared by milling starch-containing material to a particle size of 0.1 - 0.5 mm. The saccharification is carried out simultaneously. The fermentation is carried out at 28 - 36, especially 32 deg C. The glucamylase is present in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The fermentation product is recovered after fermentation. The process is carried out in the presence of a protease (preferably acid protease, especially fungal acid protease). The starch-containing material is obtained from tubers, roots, stems, seeds or whole grains of corn, cobs, wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice or potates (preferably cereals). The method of the invention is for producing fermentation product e.g. alcohol, such as ethanol selected from fuel ethanol, porabe ethanol and industrial ethanol. The method produces fermentation product without gelatinization of the starch-containing material, and produces ethanol in higher yield.

XX
CC This sequence represents an acid alpha-amylase which was used in the method of the invention. The method for producing a fermentation product from milled starch-containing material involves: saccharifying milled starch-containing material with the glucamylase from the fungi *Athelia rolfsii*, at temperature below the initial gelatinization temperature of starch containing material; and fermenting using a fermenting medium. The process is carried out for 1 - 250, especially 80 - 110 hours, at pH of 3 - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 - 55 (preferably 25 - 40, especially 30 - 35) wt. %. The sugar concentration is kept below 3 wt. % during saccharification and fermentation. A slurry of water and milled starch-containing material is prepared before step (a). The milled starch-containing material is prepared by milling starch-containing material to a particle size of 0.1 - 0.5 mm. The saccharification is carried out simultaneously. The fermentation is carried out at 28 - 36, especially 32 deg C. The glucamylase is present in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The fermentation product is recovered after fermentation. The process is carried out in the presence of a protease (preferably acid protease, especially fungal acid protease). The starch-containing material is obtained from tubers, roots, stems, seeds or whole grains of corn, cobs, wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice or potates (preferably cereals). The method of the invention is for producing fermentation product e.g. alcohol, such as ethanol selected from fuel ethanol, porabe ethanol and industrial ethanol. The method produces fermentation product without gelatinization of the starch-containing material, and produces ethanol in higher yield.
XX
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XX
SQ Sequence 484 AA:
XX
Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 LSASWRITOSIYFLIDTDRGFTNSTATCNGTNTYCGSMQGIDILDYTEGNGFTAI 60
Db 1 LSASWRITOSIYFLIDTDRGFTNSTATCNGTNTYCGSMQGIDILDYTEGNGFTAI 60
Qy 61 WISPKTEOLPQDIADEGAYHGTWQKRYDYNNSPCTADNLKSLSDALHARGYLWDVVP 120
Db 61 WISPKTEOLPQDIADEGAYHGTWQKRYDYNNSPCTADNLKSLSDALHARGYLWDVVP 120
Qy 121 DHMGAGNCNDVYDVSIFDOPDSSSYPHPYCLITIDNLTMDVCDMEGDTIVSLPDLDTTE 180
Db 121 DHMGAGNCNDVYDVSIFDOPDSSSYPHPYCLITIDNLTMDVCDMEGDTIVSLPDLDTTE 180
Qy 181 TAVRTIWWDVADLYSNTSVGDLRIDSYLEVOPDPGPYNAQGVYCVEIDGNIPASDC 240
Db 181 TAVRTIWWDVADLYSNTSVGDLRIDSYLEVOPDPGPYNAQGVYCVEIDGNIPASDC 240
Qy 241 PYQVLDGEVLYPIWQLYAPFESSGSLSYNNMNIKSVASDSCPPLGPNFENHDNPR 300
Db 241 PYQVLDGEVLYPIWQLYAPFESSGSLSYNNMNIKSVASDSCPPLGPNFENHDNPR 300
Qy 301 PAKTSDYSQAKNVLSYIPLSGIPIVYAGEQHYAGGKVYPNRAETWLGSYDTSALELYT 360
Db 301 PAKTSDYSQAKNVLSYIPLSGIPIVYAGEQHYAGGKVYPNRAETWLGSYDTSALELYT 360
Qy 361 WATTNATRKLAIAADSAYTIVANDAFTDSENITMAKGTSGSQUTLWSKGSSSSYT 420
Db 361 WATTNATRKLAIAADSAYTIVANDAFTDSENITMAKGTSGSQUTLWSKGSSSSYT 420
Qy 421 LTLSGGTTSGKLLBATCCTSYTVTDSSGDPVPMASCPRLVLPASYVDSSSLCGSGGR 480
Db 421 LTLSGGTTSGKLLBATCCTSYTVTDSSGDPVPMASCPRLVLPASYVDSSSLCGSGGR 480

XX
CC This sequence represents an acid alpha-amylase which was used in the method of the invention. The method for producing a fermentation product from milled starch-containing material involves: saccharifying milled starch-containing material with the glucamylase from the fungi *Athelia rolfsii*, at temperature below the initial gelatinization temperature of starch containing material; and fermenting using a fermenting medium. The process is carried out for 1 - 250, especially 80 - 110 hours, at pH of 3 - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 - 55 (preferably 25 - 40, especially 30 - 35) wt. %. The sugar concentration is kept below 3 wt. % during saccharification and fermentation. A slurry of water and milled starch-containing material is prepared before step (a). The milled starch-containing material is prepared by milling starch-containing material to a particle size of 0.1 - 0.5 mm. The saccharification is carried out simultaneously. The fermentation is carried out at 28 - 36, especially 32 deg C. The glucamylase is present in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The fermentation product is recovered after fermentation. The process is carried out in the presence of a protease (preferably acid protease, especially fungal acid protease). The starch-containing material is obtained from tubers, roots, stems, seeds or whole grains of corn, cobs, wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice or potates (preferably cereals). The method of the invention is for producing fermentation product e.g. alcohol, such as ethanol selected from fuel ethanol, porabe ethanol and industrial ethanol. The method produces fermentation product without gelatinization of the starch-containing material, and produces ethanol in higher yield.

XX
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RESULT 5

AC EAC92136 standard; protein: 484 AA.

ID AEC92136

DB Protein sequence of alpha amylase B.

XX
AC AEC92136;
XX
DT 01-DEC-2005 (first entry)
XX
DB WO200502015-A2.
XX
AC AEC92136;
XX
DT 06-OCT-2005.
XX
DB 18-MAR-2005; 2005WO-US009228.
XX
AC AEC92136;
XX
DT 19-MAR-2004; 2004US-0554615P.
XX
DB PR 19-MAR-2004; 2004US-0554615P.

PR 28-MAY-2004; 2004US-0575133P.

XX (NOVO) NOVOZYMES NORTH AMERICA INC.

PA (NOVO) NOVOZYMES AS.

PA

PI Bhargava, S., Bisgaard-Frantzen H., Friener H., Vikso-Nielsen A.; Johal M.; XX

DR WPI; 2005-676933/65.

XX PT Liquefying starch-containing material by treating the starch-containing material with a bacterial alpha-amylase at set temperatures and for a defined period of time.

XX PS Claim 15; SEQ ID NO 1; 30pp; English.

XX CC The new invention relates to a method of liquefying starch-containing material by treating the material with a bacterial alpha-amylase at a temperature around 70-90 degrees C for 15-90 minutes; and treating the material with an alpha-amylase at a temperature between 60-80 degrees C for 30-90 minutes. Also claimed are a process of producing a fermentation product from starch-containing material; and a process of producing syrup from starch-containing material. The starch-containing material comprises tubers, roots and/or whole grain, obtained from cereals such as corn, cob, wheat, barley, rye, milo and/or potatoes. The bacterial alpha-amylase is derived from *Bacillus stearothermophilus* alpha -amylase or a variant with the mutations: I181+G182 especially I181+G181+N193F. The alpha-amylase is an acid alpha-amylase, preferably an acid fungal alpha-amylase, preferably derived from *Aspergillus niger* or *Aspergillus oryzae*. The acid alpha-amylase is SEQ ID NO: 1. The method further comprises recovering the fermentation product, which is ethanol. The methods are useful for producing syrup from starch-containing material. The syrup is glucose, maltose, fructose syrups, malto-oligosaccharides or isomalto-oligosaccharides. The method is useful in liquefying starch-containing material for producing a fermentation product, preferably ethanol, or syrup, preferably glucose, maltose, fructose syrups, malto-oligosaccharides or isomalto-oligosaccharides. The present sequence is the protein sequence of alpha amylase B.

XX SQ Sequence 484 AA;

Qy Query Match Score 2585; DB 9; Length 484;

Best Local Similarity 100.0%; Pid. No. 3.9e-190;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LSASMRQTQIYFLTDREFRTNSTATCNGTNEIYCGGSNQGIDIDLDEGKPTAI 60

Db 1 LSASMRQTQIYFLTDREFRTNSTATCNGTNEIYCGGSNQGIDIDLDEGKPTAI 60

Qy 61 WISPITEQLQDFTADGEAYWQKQIYDVNSNFADNLKSLSDALHARGYLAVDVP 120

Db 61 WISPITEQLQDFTADGEAYWQKQIYDVNSNFADNLKSLSDALHARGYLAVDVP 120

Qy 121 DHMGYAGCNGIDVDSYVDFPDSSSYPHYCLIDWNLTMEDCNGDTIVSLPDLATE 180

Db 121 DHMGYAGCNGIDVDSYVDFPDSSSYPHYCLIDWNLTMEDCNGDTIVSLPDLATE 180

Qy 181 TAVRTINYDVAIDLVSYSVDGLRIDSYLEQDPFPGYNKASGYCYCGETDGNPASDC 240

Db 181 TAVRTINYDVAIDLVSYSVDGLRIDSYLEQDPFPGYNKASGYCYCGETDGNPASDC 240

Qy 241 PYQKVLGULNQYDLYQQLXAPSSSGSISNLXNMKSVASDCSDPLLGNPTEHNDPVR 300

Db 241 PYQKVLGULNQYDLYQQLYAFSSSGSISNLXNMKSVASDCSDPLLGNPTEHNDPVR 300

CC 301 PAKTSYDQSQRNVLSYFLTSQGIPVYAGEQHYAGGKVPNRATMUSGYDTSAELEYT 360

Db 301 PAKTSYDQSQRNVLSYFLTSQGIPVYAGEQHYAGGKVPNRATMUSGYDTSAELEYT 360

Qy 361 WIATTNAIRKLIAAADSATVYTANDAPYTDSTIAMIAGTGSQVITYLNSRKGSSGSSYT 420

Db 361 WIATTNAIRKLIAAADSATVYTANDAPYTDSTIAMIAGTGSQVITYLNSRKGSSGSSYT 420

Qy 421 LTLSGGTGTGKTLIEAVTCSTVTDSSGDPFVPHASGLPRLLPASVVDSSILCGSGR 480

Db 421 LTLSGGTGTGKTLIEAVTCSTVTDSSGDPFVPHASGLPRLLPASVVDSSILCGSGR 480

Qy 481 LYVE 484

Db 481 LYVE 484

RESULT 6

ID AEE27339 standard, protein: 484 AA.

XX AEE27339;

AC AEE27339;

DT 09-FEB-2006 (first entry)

DE Fungal acid alpha-amylase B protein sequence.

XX XX

KW fermentation; ethanol; fuel; acid alpha-amylase;

XX KW 1,4-alpha-D-glucan glucanohydrolase; enzyme; E.C 3.2.1.1.

XX OS *Aspergillus niger*.

XX OS

PN WO2005113785-A2.

XX PD 01-DEC-2005.

XX PP 11-MAY-2005; 2005WO-US016390.

XX PR 13-MAY-2004; 2004US-0570727P.

XX PR 01-DEC-2004; 2004US-0632201P.

XX PR 03-DEC-2004; 2004US-0633293P.

XX PA (NOVO) NOVOZYMES NORTH AMERICA INC.

XX PA (NOVO) NOVOZYMES AS.

XX PI Bhargava S., Friener H., Bisgaard-Frantzen H., Tams JW.

XX DR WPI: 2006-010609/01.

XX SWISSPROT; P56271.

XX PR Producing a fermentation product (preferably ethanol) from a starch-containing material, comprises treatment with alpha-amylase, and then alpha-glucosidase, before fermentation with a fermenting organism.

XX X

XX Claim 11; SEQ ID NO 1; 54pp; English.

CC The new invention relates to a method of Producing (M1) a fermentation product from starch-containing materials. The method comprises subjecting starch-containing material to an alpha-amylase, subjecting the obtained material to an alpha-glucosidase and optionally a glucose-generating and/or maltose-generating enzyme, and fermenting the material in the presence of a fermenting organism. In (M1), the fermentation product is recovered after fermentation, preferably by distillation. (M1) is useful for producing a fermentation product from starch-containing materials, where the fermentation product is ethanol, which is useful as e.g. fuel.

SCORE Search Results Details for Application 10797393 and Search Result 20070118_073134_us-10-7-393a-1.rup.

Score Home | Page Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10797393 and Search Result

20070118_073134_us-10-797-393a-1.rup.
start | next page[Go Back to previous page](#)

OM protein - Protein search, using sw model

Perfect score: 2885

Sequence: 1 LSAASRKRSTQSYFLLTDRFG.....PASVVDSSSLCCGSGRLYVE 484

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 2849598 seqs. 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2585	100.0	484	1 AMYA_ASPPG	P56271 aspergillus
2	2427	93.9	640	2 O13396_ASPPA	O13396 aspergillus
3	2390.5	92.5	634	2 Q76196_ASPPW	Q76196 aspergillus
4	1940.5	75.1	630	2 Q4WTS5_ASPPU	Q4WTS5 aspergillus
5	1780	68.9	499	2 Q7LV45_ASPPL	Q7LV45 aspergillus
6	1780	68.9	499	2 Q96TH4_ASPOR	Q96TH4 aspergillus
7	1778	68.8	498	2 Q76CT3_ASPPA	Q76CT3 aspergillus
8	1778	68.8	499	1 AMYA_ASPPR	P10329 aspergillus

http://es/ScoreAccessWeb/GetItem.action?ApplId=10797393&seqId=1052217&itemName=20070118_07...

9	1778	68.8	499	2 Q216K7_ASPPR	Q216K7 aspergillus
10	1774	68.6	499	2 Q76199_ASPPW	Q76199 aspergillus
11	1772	68.5	499	1 AMYA_ASPPAN	AMYA_ASPPAN
12	1771	68.5	498	1 AMYA_ASPPAN	AMYA_ASPPAN
13	1769	68.4	499	1 AMYA_ASPPU	AMYA_ASPPU
14	1701.5	65.8	494	2 Q4VPO9_ASPPU	Q4VPO9_aspergillus
15	1670	64.6	623	2 Q9UV09_EMENI	Q9UV09 emericella
16	1670	64.6	623	2 Q5B188_ASPPR	Q5B188 aspergillus
17	1578	61.0	490	2 Q9UV07_EMENI	Q9UV07 emericella
18	1578	61.0	490	2 Q5B2R2_EMENI	Q5B2R2 aspergillus
19	1453	56.2	647	2 Q6YJ33_LIPST	Q6YJ33 lipomyces s
20	1425	55.1	624	1 AMYV1_LIPSKO	Q01117 lipomyces k
21	1387	53.7	507	1 AMYV2_DEBLOC	Q08806 debaryomyce
22	1304.5	50.5	512	1 AMYV1_DEBLOC	P11269 debaryomyce
23	1291.5	50.0	494	1 AMYV1_SACIFI	P21567 saccharomyce
24	1247	48.2	631	2 Q92394_9HETE	Q92394 cryptococcus
25	1151	44.5	561	2 Q4X0H4_ASPPU	Q5B2F6 aspergillus
26	1146	44.3	549	2 Q2USS_ASPPU	Q2USS aspergillus
27	1131.5	43.8	492	2 Q7SD16_NEUDCR	Q7adj6 neurospora
28	1115.5	43.2	568	2 Q4V135_ASPPU	Q4v135 aspergillus
29	1098.5	42.5	521	2 Q5BA4M3_EMENI	Q5Bam3 aspergillus
30	1090.5	42.2	559	2 Q5AZF6_EMENI	Q5azf6 aspergillus
31	1088	42.1	552	2 Q5B822_EMENI	Q5B822 aspergillus
32	1062	41.1	561	2 Q4WFV4_ASPPU	Q4wf4 aspergillus
33	1061.5	41.1	532	2 Q2KHCO_MACGR	Q2khco magnaporthe
34	1057	40.9	532	2 Q5SS33_CRYNE	Q5ss33 cryptococcus
35	1057	40.9	532	2 Q5KG16_CRYNE	Q5kg16 cryptococcus
36	1001	38.7	533	2 Q784K0_NEUDCR	Q784k0 neurospora
37	908	35.1	513	1 AMY1_SCHPQ	Q14154 schizosaccharomyces
38	903.5	35.0	572	2 Q55KB2_CRYNE	Q55kb2 cryptococcus
39	902.5	34.9	572	2 Q5K993_CRYNE	Q5k993 schizosaccharomyces
40	901	34.9	625	2 Q74922_SCIRHO	Q74922 schizosaccharomyces
41	852.5	33.0	564	1 AMY4_SKRPO	Q97799 schizosaccharomyces
42	845	32.7	460	2 Q4T16_GIBBEZ	Q4t16 gibberella
43	837.5	32.4	561	2 Q5PKY6_CRYNE	Q5pk6 cryptococcus
44	835.5	32.3	600	2 Q2KE07_MAGGR	Q2keq magnaporthe
45	832	32.2	460	2 Q3YBZ7_GIBMO	Q3yb7 gibberella

ALIGNMENTS

RESULT 1	AMYA_ASPPG	STANDARD:	PRT:	484 AA.
ID	AMYA_ASPPG			
AC	P56271;			
DR	15-JUL-1998. Integrated into UniProtKB/Swiss-Prot.			
DR	15-JUL-1998. sequence version 1.			
DR	07-FEB-2006. entry version 34.			
DR	Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).			
DS	Aspergillus niger. Fungi: Ascomycota: Pezizomycotina: Eurotiomycetes; OS			
OC	Eukaryota: Fungi: Ascomycota: Pezizomycotina: Eurotiomycetes; OC			
OC	Eurotiomycetes: Trichocomaceae; mitosporic trichocomaceae; Aspergillus.			
NCBI_TaxID	5061;			
RN				
RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).			
RX	MEDLINE:91062514; PubMed:2207059;			
RA	Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,			
RA	Jensen V.J., Petersen S.B., Swift H., Thimm L., Woldike H.P.;			
RA	*Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-			
RT	A resolution of two enzymes from Aspergillus.;"			
RL	Biochemistry 20:6244-6249 (1990).			
CC	-- CATALYTIC ACTIVITY: Endohydrolase: 1,4-alpha-D-glucosidic linkages in oligosaccharides and polysaccharides.			
CC	-- BINDING: Calcium ions per subunit. Calcium is inhibitory			

CC at high concentrations.
 CC -:- SUBONI: Monomers.
 CC -:- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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 CC
 DR PDB: 2AAA; X-ray; Q=1.484.
 DR LinkHub; P56271;
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR Pfam: PP00121; Alpha-amylase_1.
 DR SMART: SM00612; Amyl_1.
 KW 3D-structure; Calcium; Carbohydrate metabolism; Glycoprotein;
 KW Glycosidase; Hydrolase; Metal-binding.
 FT CHAIN 1 484 /Pfam-PRO_000004289.
 FT ACT_SITE 206 206 Acid alpha-amylase.
 FT ACT_SITE 230 230 Nucleophile.
 FT ACT_SITE 297 297 Proton donor.
 FT METAL 121 121 Calcium 1.
 FT METAL 162 162 Calcium 1 (via carbonyl oxygen).
 FT METAL 175 175 Calcium 1.
 FT METAL 206 206 Calcium 2.
 FT METAL 210 210 Calcium 1 (via carbonyl oxygen).
 FT METAL 230 230 Calcium 2.
 FT CARBOHYD 24 24 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 157 157 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 197 197 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 30 38
 FT DISULFID 150 164
 FT DISULFID 240 283
 FT DISULFID 440 475
 FT HELIX 3 6
 FT TURN 7 8
 FT STRAND 11 13
 FT HELIX 16 19
 FT TURN 22 23
 FT STRAND 26 26
 FT HELIX 32 34
 FT STRAND 36 36
 FT HELIX 42 47
 FT TURN 48 48
 FT HELIX 49 53
 FT TURN 54 56
 FT STRAND 59 62
 FT STRAND 66 68
 FT STRAND 73 73
 FT TURN 74 75
 FT STRAND 76 76
 FT TURN 78 78
 FT STRAND 79 80
 FT STRAND 81 81
 FT STRAND 83 83
 FT TURN 92 94
 FT HELIX 97 108
 FT TURN 109 111
 FT STRAND 113 118
 FT STRAND 121 122
 FT STRAND 125 127
 FT HELIX 129 131
 FT HELIX 134 136
 FT STRAND 137 139
 FT STRAND 142 142
 FT HELIX 143 145

FT	STRAND	146	146
FT	TURN	151	151
FT	HELIX	155	156
FT	STRAND	158	163
FT	STRAND	164	167
FT	STRAND	169	173
FT	STRAND	175	176
FT	TURN	178	179
FT	STRAND	180	180
FT	HELIX	181	195
FT	TURN	199	199
FT	STRAND	202	206
FT	STRAND	208	208
FT	TURN	209	210
FT	STRAND	211	211
FT	HELIX	213	223
FT	TURN	224	224
FT	STRAND	225	229
FT	STRAND	234	234
FT	HELIX	236	244
FT	TURN	245	245
FT	STRAND	246	250
FT	HELIX	252	262
FT	STRAND	263	264
FT	TURN	265	266
FT	STRAND	267	267
FT	HELIX	269	282
FT	STRAND	284	284
FT	HELIX	286	286
FT	STRAND	289	291
FT	TURN	293	293
FT	STRAND	296	297
FT	STRAND	298	298
FT	HELIX	301	303
FT	TURN	304	304
FT	HELIX	308	320
FT	STRAND	321	328
FT	TURN	329	334
FT	TURN	339	343
FT	HELIX	347	350
FT	TURN	351	352
FT	TURN	354	355
FT	HELIX	357	375
FT	TURN	377	381
FT	STRAND	382	382
FT	STRAND	385	390
FT	TURN	391	392
FT	STRAND	393	400
FT	TURN	401	403
FT	STRAND	405	410
FT	STRAND	412	412
FT	TURN	414	415
FT	STRAND	416	416
FT	STRAND	419	423
FT	TURN	430	431
FT	STRAND	432	436
FT	TURN	437	438
FT	STRAND	439	444
FT	TURN	447	448
FT	STRAND	449	449
FT	STRAND	451	455
FT	TURN	457	458
FT	STRAND	461	465
FT	HELIX	466	469
FT	TURN	470	471